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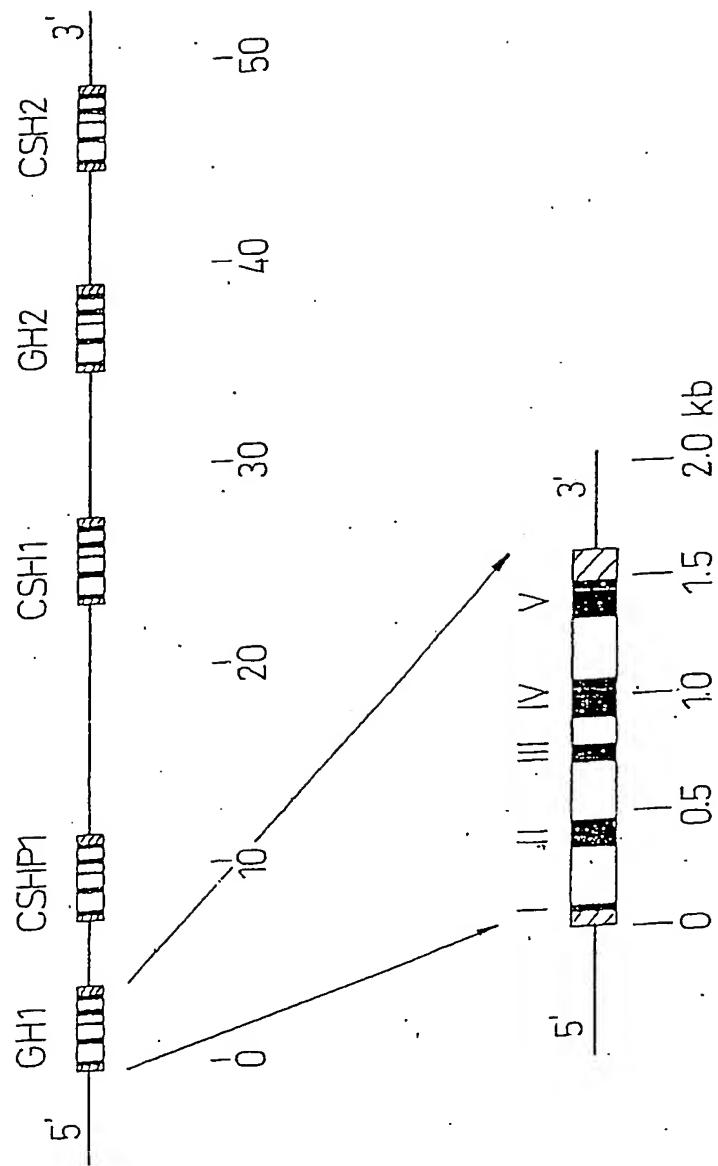


Fig. 1

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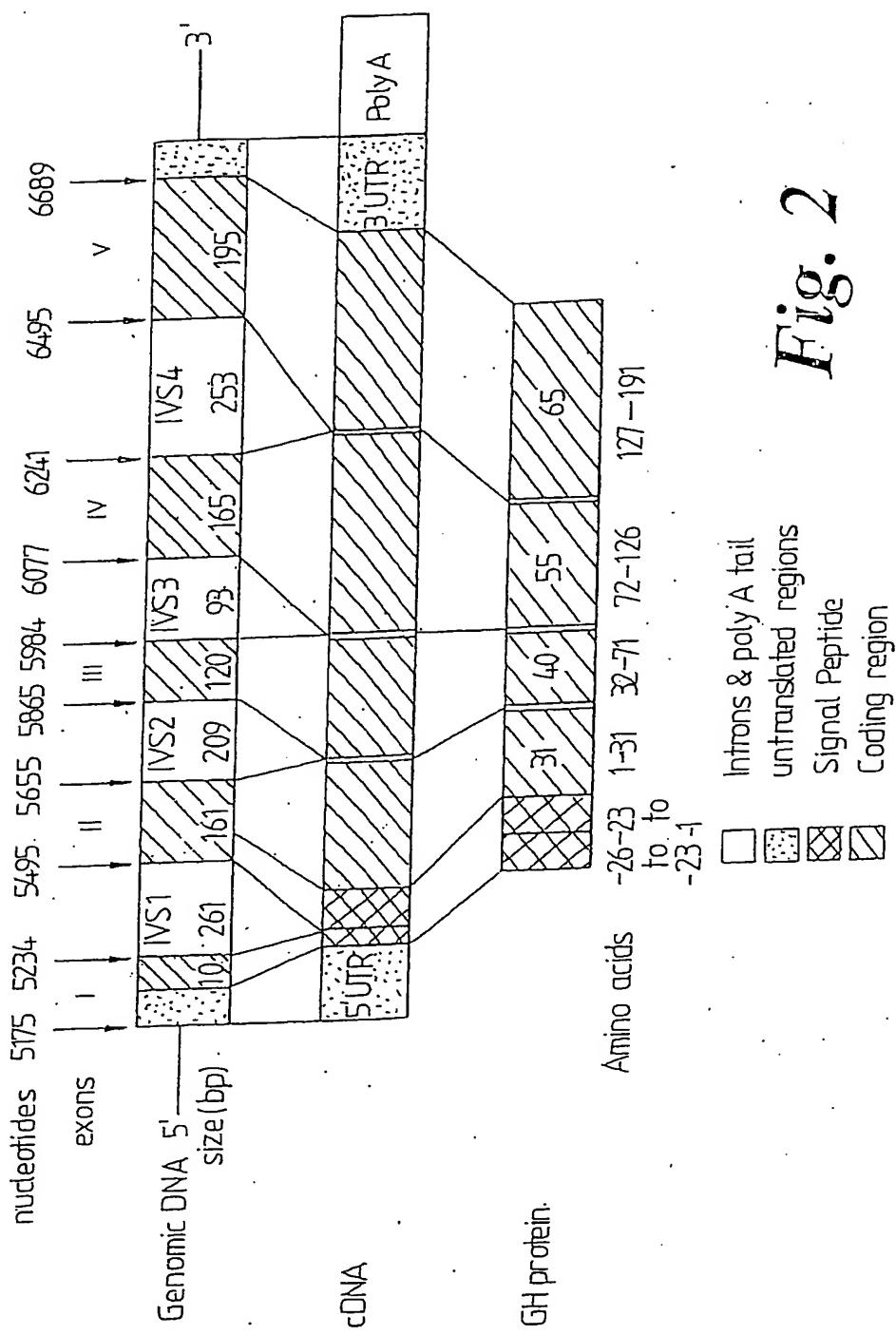


Fig. 2

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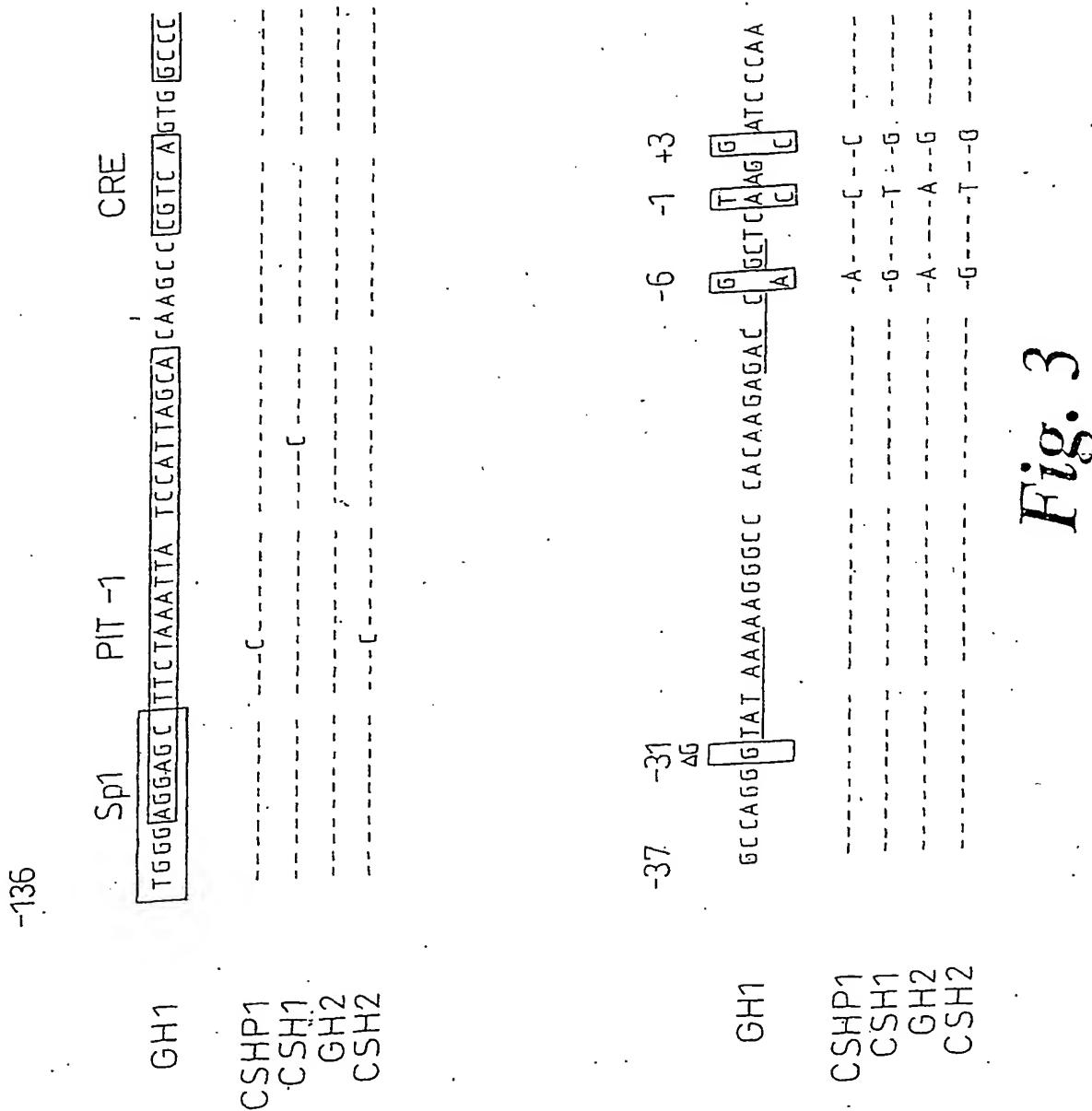


FIGURE 4

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-200 tcacaacact ggtaacgggtt gtaaggggaaa gatgacaaggc cagggggcat -151
-150 gatccagca tggtagggag gagtttttaa attatccatt agcacaaggcc -101
-100 cgtcgtggc cccatgtcata aatgtacaca gaaacagggtt gggcaacag -51
-50 tggagagaa gggccagggtt tataaaagg gcccacaaga gaccaggctca -1
+1 agatcccaa ggccaaactc cccgaaaccac tcaggltctt gtggacagct +50
+51 caccttagcg caatggctac aggttaagcggc cccttaaaatc ccgttggca +100
+101 caatgtgtcc tgaggggaga ggcaaggcacc tgtagatggg acggggggcac +150
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FIGURE 5

Growth hormone 1

Gene symbol : GH1

Location : 17q

1	2						
-26	ATG GCT ACA G ₁ GC TCC CGG ACG TCC CTC CTG GCT CTC GCT GGC CTC	-12					
Met Ala Thr G ₁ ly Ser Arg Thr Ser Leu Leu Ala Phe Gly Leu							
-11	CTC TGC CTC CCC TGG CTT CAA GAG GGC AGT GGC TTC CCA ACC ATT	4					
Leu Cys Leu Pro Trp Leu Gln Glu Gly Ser Ala Phe Pro Thr Ile							
5	CCC TTA TCC AGG CTT TTT GAC AAC GCT ATG CTC CGC GCC CAT CGT	19					
Pro Leu Ser Arg Leu Phe Asp Asn Ala Met Leu Arg Ala His Arg	2 3						
20	CTG CAC CAG CTG GCC TTT GAC ACC TAC CAG GAG TTT ↓ GAA GAA GCC	34					
Leu His Gln Leu Ala Phe Asp Thr Tyr Gln Glu Phe Glu Glu Ala							
35	TAT ATC CCA AAG GAA CAG AAG TAT TCA TTC CTG CAG AAC CCC CAG	49					
Tyr Ile Pro Lys Glu Gln Lys Tyr Ser Phe Leu Gln Asn Pro Gln							
50	ACC TCC CTC TGT TTC TCA GAG TCT ATT CCG ACA CCC TCC AAC AGG	64					

Thr Ser Leu Cys Phe Ser Glu Ser Ile Pro Thr Pro Ser Asn Arg

3 4

65 GAG GAA ACA CAA CAG AAA TCC ↓ AAC CTA GAG CTG CTC CGC ATC TCC 79
Glu Glu Thr Gln Gln Lys Ser Asn Leu Glu Leu Leu Arg Ile Ser

80 CTG CTG CTC ATC CAG TCG CTG TGG CTG GAG CCC GTG CAG TTC CTC AGG 94
Leu Leu Ile Gln Ser Trp Leu Glu Pro Val Gln Phe Leu Arg

95 AGT GTC TTC GCC AAC AGC CTG GTG TAC GGC GCC TCT GAC AGC AAC 109
Ser Val Phe Ala Asn Ser Leu Val Tyr Gly Ala Ser Asp Ser Asn

110 GTC TAT GAC CTC CTA AAG GAC CTA GAG GAA GGC ATC CAA ACG CTG 124
Val Tyr Asp Leu Leu Lys Asp Leu Glu Glu Gly Ile Gln Thr Leu

4 5

125 ATG GGG ↓ AGG CTG GAA GAT GGC AGC CCC CGG ACT GGG CAG ATC TTG 139
Met Gly Arg Leu Glu Asp Gly Ser Pro Arg Thr Gly Gln Ile Phe

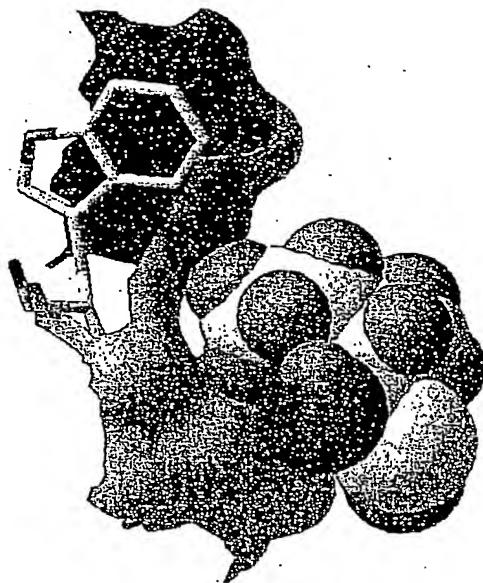
140 AAG CAG ACC TAC AGC AAG TTC GAC ACA AAC TCA CAC AAC GAT GAC 154
Lys Gln Thr Tyr Ser Lys Phe Asp Thr Asn Ser His Asn Asp Asp

155 GCA CTC AAC TAC GGG CTG CTC TAC TGC TTC AGG AAG GAC 169
Ala Leu Lys Asn Tyr Gly Leu Leu Tyr Cys Phe Arg Lys Asp

170 ATG GAC AAG GTC GAG ACA TTC CTG CGC ATC GTG CAG TGC CGC TCT 184
Met Asp Lys Val Glu Thr Phe Leu Arg Ile Val Gln Cys Arg Ser

185 GTG GAG GGC AGC TGT GGC TTC TAG
Val Glu Gly Ser Cys Gly Phe *

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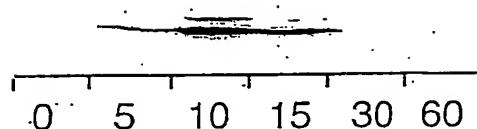
The tight interaction between the side chain of GH residue Ile179 and GHR residue Trp169.

The Ile179 residue is depicted by a space filling model. Trp169 is represented as a stick model whilst the molecular surface of GHR residues 167-169 is shown in green

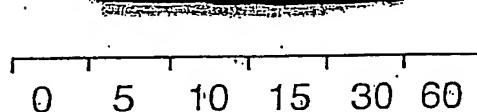
FIGURE 6

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A ERK



B STAT5



C

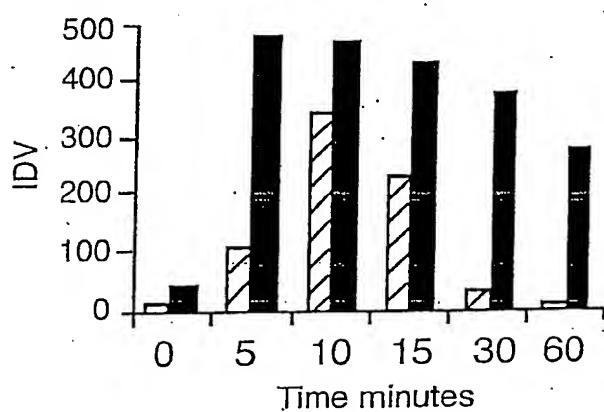


FIGURE 7

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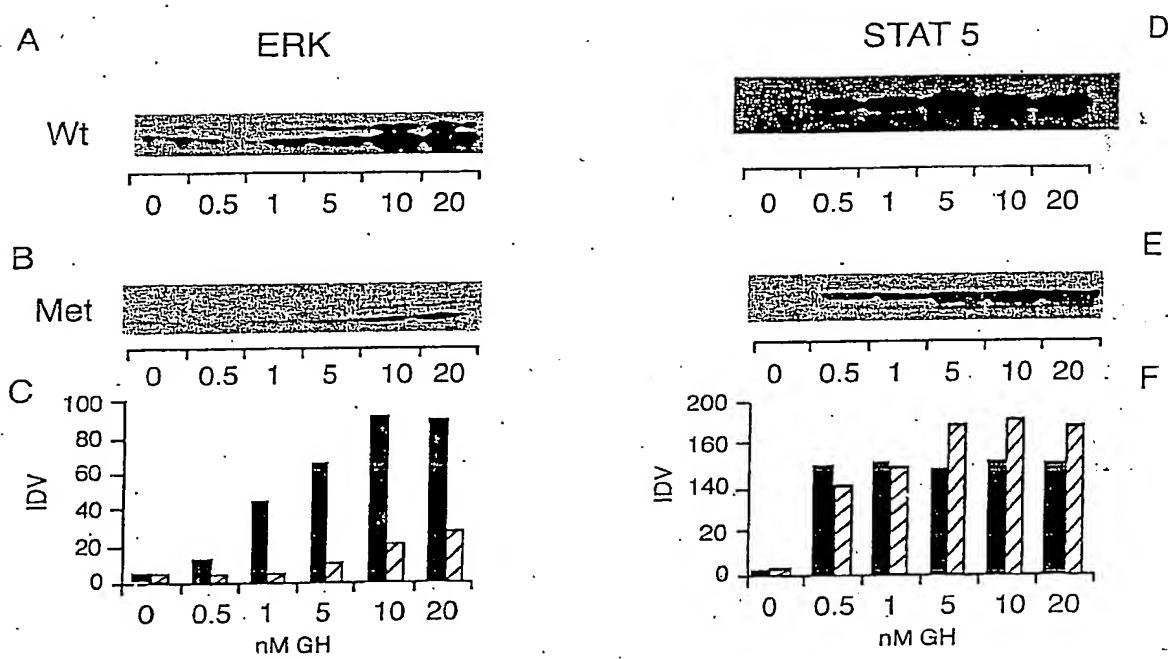


FIGURE 8

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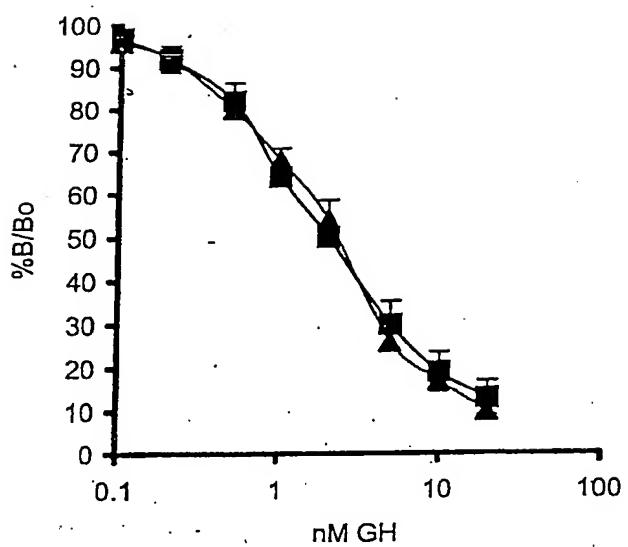


FIGURE 9

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